Search Results -

Terms	Documents
L1 same (carbohydrate binding domain)	2

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Search: L7

Refine Search

Recall Text | Clear

Search History

DATE: Tuesday, January 07, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L7	L1 same (carbohydrate binding domain)	2	L7
L6	L1 same (carbohydrate binding domain) or CBD	667	L6
L5	L1 same multidomain	7	L5
L4	L1 and cellulolyticus	10	L4
L3	L1 same cellulolyticus	0	L3
L2	L1 same (Acidothermus or cellulolyticus)	0	L2
L1	mannanase	449	L1

END OF SEARCH HISTORY

=> d l13 ibib ab 1-5

L13 ANSWER 1 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 2000-0125777 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2000 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): A gene encoding a novel **multidomain** .beta.-1,4-**mannanase** from Caldibacillus cellulovorans and action of the recombinant enzyme on kraft pulp
AUTHOR: SUNNA A.; GIBBS M. D.; CHIN C. W. J.; NELSON P. J.; BERGQUIST P. L.
CORPORATE SOURCE: Department of Biological Sciences, Macquarie University, Sydney, New South Wales 2109, Australia; CSIRO Forestry and Forest Products, Clayton, Victoria 3168, Australia; Department of Molecular Medicine, University of Auckland Medical School, Auckland, New Zealand
SOURCE: Applied and environmental microbiology : (Print), (2000), 66(2), 664-670, 49 refs.
ISSN: 0099-2240 CODEN: AEMIDF
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7195, 354000081943430300
AB Genomic walking PCR was used to obtained a 4,567-bp nucleotide sequence from Caldibacillus cellulovorans. Analysis of this sequence revealed that there were three open reading frames, designated ORF1, ORF2, and ORF3. Incomplete ORF1 encoded a putative C-terminal cellulose-binding domain (CBD) homologous to members of CBD family IIIb, while putative ORF3 encoded a protein of unknown function. The putative **ManA** protein encoded by complete **manA** ORF2 was an enzyme with a novel **multidomain** structure and was composed of four domains in the following order: a putative N-terminal domain (D1) of unknown function, an internal CBD (D2), a .beta.-**mannanase** catalytic domain (D3), and a C-terminal CBD (D4). All four domains were linked via proline-threonine-rich peptides. Both of the CBDs exhibited sequence similarity to family IIIb CBDs, while the **mannanase** catalytic domain exhibited homology to the family 5 glycosyl hydrolases. The purified recombinant enzyme ManAd3 expressed from the cloned catalytic domain (D3) exhibited optimum activity at 85.degree.C and pH 6.0 and was extremely thermostable at 70.degree.C. This enzyme exhibited high specificity with the substituted galactomannan locust bean gum, while more substituted galacto- and glucomannans were poorly hydrolyzed. Preliminary studies to determine the effect of the recombinant ManAd3 and a recombinant thermostable .beta.-xylanase on oxygen-delignified Pinus radiata kraft pulp revealed that there was an increase in the brightness of the bleached pulp.

L13 ANSWER 2 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 1996-0344081 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1996 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Sequencing, cloning and expression of a .beta.,1- 4-**mannanase** gene, **manA**, from the extremely thermophilic anaerobic bacterium, Caldicellulosiruptor Rt8B.4
AUTHOR: GIBBS M. D.; ELINDER A. U.; REEVES R. A.; BERGQUIST P. L.
CORPORATE SOURCE: Centre for Gene Technology, School of Biological Sciences, University of Auckland, Private Bag 92019, Auckland, New Zealand
SOURCE: FEMS microbiology letters, (1996), 141(1), 37-43, 20

refs.
ISSN: 0378-1097 CODEN: FMLED7
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Netherlands
LANGUAGE: English
AVAILABILITY: INIST-17567A, 354000060287330060
AB A gene encoding a .beta.-**mannanase** (**manA**) has been cloned from an obligately anaerobic extreme thermophile, Caldicellulosiruptor strain Rt8B.4, which is most closely related to Caldicellulosiruptor saccharolyticus (formerly Caldocellum saccharolyticum). The gene codes for a **multidomain** enzyme with a C-terminal .beta.-**mannanase** domain which was amplified by the polymerase chain reaction and cloned into a temperature-inducible expression vector in Escherichia coli. Sequence comparisons have shown that the Man domain of Rt8B.4 **ManA** is related to a thermophilic Dictyoglomus **mannanase** and a mesophilic **mannanase** from a Bacillus species. It appears to be unrelated to the .beta.-**mannanase** domain of C. saccharolyticus, implying acquisition of the genes from unrelated sources by the two bacteria.

L13 ANSWER 3 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 1995-0408085 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1995 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Correction of the .beta.-**mannanase** domain of the celC pseudogene from Caldocellulosiruptor saccharolyticus and activity of the gene product on kraft pulp
AUTHOR: MORRIS D. D.; REEVES R. A.; GIBBS M. D.; SAUL D. J.; BERGQUIST P. L.
CORPORATE SOURCE: Univ. Auckland, school biological sci., cent. gene technology, Auckland, New Zealand
SOURCE: Applied and environmental microbiology, (1995), 61(6), 2262-2269, 39 refs.
ISSN: 0099-2240 CODEN: AEMIDF
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7195, 354000050861870300
AB The celA, **manA**, and celB genes from Caldocellulosiruptor saccharolyticus compose a cellulase-hemicellulase gene cluster and are arranged on a 12-kb C. saccharolyticus genomic fragment of the recombinant lambda bacteriophage NZP.lambda.2. The beginning of a fourth open reading frame (celC) which was homologous to the C. saccharolyticus **manA** and celA genes was located at the 3' end of the 12-kb NZP.lambda.2 genomic fragment. Genome-walking PCR was used to isolate DNA fragments downstream of the C. saccarolyticus celB gene, and the entire nucleotide sequence of celC was obtained. From the preliminary nucleotide sequence, celC appeared to encode yet another **multidomain** bifunctional enzyme (CelC) consisting of an N-terminal endo-1,4-.beta.-D-glucanase domain (75% similar to CelA domain 1), two central cellulose-binding domains, and a C-terminal endo-1,4-.beta.-D-**mannanase** domain (98% similar to **ManA** domain 1). However, upon completion of the celC sequencing, two -1 frameshifts were identified in the region encoding the putative CelC **mannanase** domain. The isolated CelC **mannanase** domain exhibited no .beta.-**mannanase** activity, which supported this observation. Recombinant PCR was used to correct the celC frameshifts by inserting the appropriate nucleotides into the gene. The repaired celC fragment containing the base insertions (manB) expressed strong .beta.-**mannanase** activity on soluble mannan substrates and showed significant activity on kraft pulp as judged by the release of reducing sugars

L13 ANSWER 4 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 1993-0161687 PASCAL
TITLE (IN ENGLISH): The .beta.-**mannanase** from Caldocellum saccharolyticum is part of a **multidomain** enzyme
AUTHOR: GIBBS M. D.; SAUL D. J.; LUETHI E.; BERGQUIST P. L.
CORPORATE SOURCE: Univ. Auckland, cent. gene technology, dep. cellular molecular biology, Auckland, New Zealand
SOURCE: Applied and environmental microbiology, (1992), 58(12), 3864-3867, 18 refs.
ISSN: 0099-2240 CODEN: AEMIDF
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7195, 354000032511890140
AB The complete sequence of a .beta.-**mannanase** gene from an anaerobic extreme thermophile was determined, and it shows that the expressed protein consists of two catalytic domains and two binding domains separated by spacer regions rich in proline and threonine residues. The amino-terminal catalytic domain has .beta.-**mannanase** activity, and the carboxy-terminal domain acts as an endoglucanase. Neither domain shows homology with any other cellulase or hemicellulase sequence at the nucleic acid or protein level

L13 ANSWER 5 OF 5 AGRICOLA
ACCESSION NUMBER: 95:41704 AGRICOLA
DOCUMENT NUMBER: IND20466272
TITLE: Correction of the beta-**mannanase** domain of the celC pseudogene from Caldocellulosiruptor saccharolyticus and activity of the gene product on kraft pulp.
AUTHOR(S): Morris, D.D.; Reeves, R.A.; Gibbs, M.D.; Saul, D.J.; Bergquist, P.L.
CORPORATE SOURCE: University of Auckland, Auckland, New Zealand.
AVAILABILITY: DNAL (448.3 Ap5)
SOURCE: Applied and environmental microbiology, June 1995. Vol. 61, No. 6. p. 2267-2269
Publisher: Washington : American Society for Microbiology
CODEN: AEMIDF; ISSN: 0099-2240
NOTE: Includes references
PUB. COUNTRY: District of Columbia; United States
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English
AB The celA, **manA**, and celB genes from Caldocellulosiruptor saccharolyticus compose a cellulase-hemicellulase gene cluster and are arranged on a 12-kb C. saccharolyticus genomic fragment of the recombinant lambda bacteriophage NZP lambda 2. The beginning of a fourth open reading frame (celC) which was homologous to the C. saccharolyticus monA and celA genes was located at the 3' end of the 12-kb NZP lambda 2 genomic fragment. Genome-walking PCR was used to isolate DNA fragments downstream of the C saccharolyticus celB gene, and the entire nucleotide sequence of celC was obtained. From the preliminary nucleotide sequence, celC appeared to encode yet another **multidomain** bifunctional enzyme (CelC) consisting of an N-terminal endo-1,4-beta-D-glucanase domain (75% similar to CeLA domain 1), two central cellulose-binding domains, and a C-terminal endo-1,4-beta-D-**mannanase** domain (98% similar to **ManA** domain 1). However, upon completion of the celC sequencing, two -1 frameshifts were identified in the region encoding the putative CelC **mannanase** domain. The isolated CelC **mannanase** domain exhibited no beta-**mannanase** activity, which supported this

observation. Recombinant PCR was used to correct the celC frameshifts by inserting the appropriate nucleotides into the gene. The repaired celC fragment containing the base insertions (manB) expressed strong beta-**mannanase** activity on soluble mannan substrates and showed significant activity on kraft pulp as judged by the release of reducing sugars.

=> d l8 ibib ab 1-5

L8 ANSWER 1 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
DUPLICATE
ACCESSION NUMBER: 2001-0058776 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): A novel thermostable **multidomain** 1,4-.beta.-xylanase from 'Caldibacillus cellulovorans' and effect of its xylan-binding domain on enzyme activity
AUTHOR: SUNNA Anwar; GIBBS Moreland D.; BERGQUIST Peter L.
CORPORATE SOURCE: Department of Biological Sciences, Macquarie University, North Ryde, Sydney, NSW 2109, Australia; Department of Molecular Medicine, University of Auckland Medical School, Private Bag 92019, Auckland, New Zealand
SOURCE: Microbiology : (Reading), (2000), 146(p.11), 2947-2955, refs. 1 p.1/4
ISSN: 1350-0872
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-4410, 354000093243780230
AB The nucleotide sequence of the complete xynA gene, encoding a novel **multidomain** xylanase XynA of 'Caldibacillus cellulovorans', was determined by genomic-walking PCR. The putative XynA comprises an N-terminal domain (D1), recently identified as a xylan-binding domain (XBD), homologous to non-catalytic thermostabilizing domains from other xylanases. D1 is followed by a xylanase catalytic domain (D2) homologous to family 10 glycosyl hydrolases. Downstream of this domain two cellulose-binding domains (**CBD**), D3 and D4, were found linked via proline-threonine (PT)-rich peptides. Both **CBDs** showed sequence similarity to family IIIb **CBDs**. Upstream of xynA an incomplete open reading frame was identified, encoding a putative C-terminal **CBD** homologous to family IIIb **CBDs**. Two expression plasmids encoding the N-terminal XBD plus the catalytic domain (XynAd1/2) and the xylanase catalytic domain alone (XynAd2) were constructed and the biochemical properties of the recombinant enzymes compared. The absence of the XBD resulted in a decrease in thermostability of the catalytic domain from 70 .degree.C (XynAd1/2) to 60 .degree.C (XynAd2). Substrate-specificity experiments and analysis of the main products released from xylan hydrolysis indicate that both recombinant enzymes act as endo-1,4-.beta.-xylanases, but differ in their ability to cleave small xylooligosaccharides.

L8 ANSWER 2 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
DUPLICATE
ACCESSION NUMBER: 2000-0125777 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2000 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): A gene encoding a novel **multidomain** .beta.-1,4-mannanase from Caldibacillus cellulovorans and action of the recombinant enzyme on kraft pulp
AUTHOR: SUNNA A.; GIBBS M. D.; CHIN C. W. J.; NELSON P. J.; BERGQUIST P. L.
CORPORATE SOURCE: Department of Biological Sciences, Macquarie University, Sydney, New South Wales 2109, Australia; CSIRO Forestry and Forest Products, Clayton, Victoria 3168, Australia; Department of Molecular Medicine, University of Auckland Medical School, Auckland, New Zealand
SOURCE: Applied and environmental microbiology : (Print),

(2000), 66(2), 664-670, 49 refs.
ISSN: 0099-2240 CODEN: AEMIDF
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7195, 354000081943430300

In IDS

AB Genomic walking PCR was used to obtained a 4,567-bp nucleotide sequence from Caldibacillus cellulovorans. Analysis of this sequence revealed that there were three open reading frames, designated ORF1, ORF2, and ORF3. Incomplete ORF1 encoded a putative C-terminal cellulose-binding domain (**CBD**) homologous to members of **CBD** family IIIb, while putative ORF3 encoded a protein of unknown function. The putative ManA protein encoded by complete manA ORF2 was an enzyme with a novel **multidomain** structure and was composed of four domains in the following order: a putative N-terminal domain (D1) of unknown function, an internal **CBD** (D2), a .beta.-mannanase catalytic domain (D3), and a C-terminal **CBD** (D4). All four domains were linked via proline-threonine-rich peptides. Both of the **CBDs** exhibited sequence similarity to family IIIb **CBDs**, while the mannanase catalytic domain exhibited homology to the family 5 glycosyl hydrolases. The purified recombinant enzyme ManAd3 expressed from the cloned catalytic domain (D3) exhibited optimum activity at 85.degree.C and pH 6.0 and was extremely thermostable at 70.degree.C. This enzyme exhibited high specificity with the substituted galactomannan locust bean gum, while more substituted galacto- and glucomannans were poorly hydrolyzed. Preliminary studies to determine the effect of the recombinant ManAd3 and a recombinant thermostable .beta.-xylanase on oxygen-delignified Pinus radiata kraft pulp revealed that there was an increase in the brightness of the bleached pulp.

L8 ANSWER 3 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 2000-0533641 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2000 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Molecular characterization of xynX, a gene encoding a **multidomain** xylanase with a thermostabilizing domain from Clostridium thermocellum
AUTHOR: KIM H.; JUNG K. H.; PACK M. Y.
CORPORATE SOURCE: Department of Agricultural Chemistry, Sunchon National University, Sunchon 540-742, Korea, Republic of; Bacterial Molecular Genetics Research Unit, Korea Research Institute of Bioscience and Biotechnology (KRIBB), P.O. Box 115, Taejon 305-600, Korea, Republic of; Department of Biological Sciences, Korea Advanced Institute of Science and Technology, Taejon 305-701, Korea, Republic of
SOURCE: Applied microbiology and biotechnology, (2000), 54(4), 521-527, 23 refs.
ISSN: 0175-7598 CODEN: AMBIDG
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
AVAILABILITY: INIST-16771, 354000092573880100

AB A Clostridium thermocellum gene, xynX, coding for a xylanase was cloned and the complete nucleotide sequence was determined. The xylanase gene of Clostridium thermocellum consists of an ORF of 3261 nucleotide encoding a xylanase (XynX) of 1087 amino acid residues (116 kDa). Sequence analysis of XynX showed a **multidomain** structure that consisted of four different domains: an N-terminal thermostabilizing domain homologous to sequences found in several thermophilic enzymes, a catalytic domain homologous to family 10 glycosyl hydrolases, a duplicated cellulose-binding domain (**CBD**) homologous to family IX

CBDs, and a triplicated S-layer homologous domain. A deletion mutant of xynX having only the catalytic region produced a mutant enzyme XynX-C which retained catalytic activity but lost thermostability. In terms of half-life at 70 .degree.C, the thermostability of XynX-C was about six times lower than that of the other mutant enzyme, XynX-TC, produced by a mutant containing both the thermostabilizing domain and the catalytic domain. The optimum temperature of XynX-C was about 5-10 .degree.C lower than that of XynX-TC.

L8 ANSWER 4 OF 5 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 2000-0434470 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2000 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): **Multidomain** and multifunctional glycosyl hydrolases from the extreme thermophile Caldicellulosiruptor isolate Tok7B. 1
AUTHOR: GIBBS M. D.; REEVES R. A.; FARRINGTON G. K.; ANDERSON P.; WILLIAMS D. P.; BERGQUIST P. L.
CORPORATE SOURCE: Department of Biological Sciences, Macquarie University, Sydney, New South Wales 2109, Australia; Clariant Corporation, Biotech Research Division, Lexington, MA 02173, United States; Department of Molecular Medicine, University of Auckland Medical School, Private Bag 92019, Auckland, New Zealand
SOURCE: Current microbiology : (Print), (2000), 40(5), 333-340, 42 refs.
ISSN: 0343-8651 CODEN: CUMIDD
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-17631, 354000087240240090
AB DNA sequencing techniques have revealed widespread molecular diversity of the genomic organization of apparently closely related bacteria (as judged from SSU rDNA sequence similarity). We have previously described the extreme thermophile Caldicellulosiruptor saccharolyticus, which is unusual in possessing multi-catalytic, **multidomain** arrangements for the majority of its glycosyl hydrolases. We report here the sequencing of three gene clusters of glycosyl hydrolases from Caldicellulosiruptor sp. strain Tok7B. 1. These clusters are not closely linked, and each is different in its organization from any described for Cs saccharolyticus. The catalytic domains of the enzymes belong to glycosyl hydrolase families 5, 9, 10, 43, 44, and 48. The cellulose binding domains (**CBDs**) of these enzymes from Caldicellulosiruptor sp. Tok7B. I are types IIIb, IIIc, or VI. A number of individual catalytic and binding domains have been expressed in Escherichia coli, and biochemical data are reported on the purified enzymes for cellulose degradation encoded by engineered derivatives of celB and celE.

L8 ANSWER 5 OF 5 CABA COPYRIGHT 2003 CABI DUPLICATE 3
ACCESSION NUMBER: 2002:158862 CABA
DOCUMENT NUMBER: 20023044458
TITLE: Functional analysis of the carbohydrate-binding domains of Erwinia chrysanthemi Cel5 (endoglucanase Z) and an Escherichia coli putative chitinase
AUTHOR: Simpson, H. D.; Barras, F.
CORPORATE SOURCE: Laboratoire de Chimie Bacterienne, Centre National de la Recherche Scientifique, 31 Chemin Joseph Aiguier, 13402 Marseille Cedex 20, France.
SOURCE: Journal of Bacteriology, (1999) Vol. 181, No. 15, pp. 4611-4616. 38 ref.
ISSN: 0021-9193
DOCUMENT TYPE: Journal

LANGUAGE: English

AB The Cel5 cellulase (formerly known as endoglucanase Z) from E. chrysanthemi is a **multidomain** enzyme consisting of a catalytic domain, a linker region, and a cellulose binding domain (**CBD**). A three-dimensional structure of the CBDCel5 has previously been obtained by nuclear magnetic resonance. In order to define the role of individual residues in cellulose binding, site-directed mutagenesis was performed. The role of three aromatic residues (Trp18, Trp43, and Tyr44) in cellulose binding was demonstrated. The exposed potential hydrogen bond donors, residues Gln22 and Glu27, appeared not to play a role in cellulose binding, whereas residue Asp17 was important for the stability of Cel5. A deletion mutant lacking the residues Asp17 to Pro23 bound only weakly to cellulose. The sequence of CBDCel5 exhibits homology to a series of five repeating domains of a putative large protein, referred to as Yheb, from Escherichia coli. One of the repeating domains (Yheb1), consisting of 67 amino acids, was cloned from the E. coli chromosome and purified by metal chelating chromatography. While CBDCel5 bound to both cellulose and chitin, Yheb1 bound well to chitin, but only very poorly to cellulose. The Yheb protein contains a region that exhibits sequence homology with the catalytic domain of a chitinase, which is consistent with the hypothesis that the Yheb protein is a chitinase.

```
=> d his

     (FILE 'HOME' ENTERED AT 13:49:11 ON 07 JAN 2003)

     INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
     DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 13:49:20 ON
     07 JAN 2003
                SEA MANNANASE
                ---------
              194   FILE AGRICOLA
                3   FILE ANABSTR
               17   FILE AQUASCI
               77   FILE BIOBUSINESS
                3   FILE BIOCOMMERCE
              544   FILE BIOSIS
              264   FILE BIOTECHABS
              264   FILE BIOTECHDS
              191   FILE BIOTECHNO
              205   FILE CABA
              880   FILE CAPLUS
               88   FILE CEABA-VTB
                2   FILE CEN
                3   FILE CIN
               15   FILE CONFSCI
                3   FILE CROPB
               11   FILE CROPU
                3   FILE DDFB
                1   FILE DDFU
              263   FILE DGENE
                3   FILE DRUGB
                1   FILE DRUGU
                3   FILE EMBAL
              184   FILE EMBASE
              188   FILE ESBIOBASE
                8   FILE FEDRIP
               52   FILE FROSTI
              145   FILE FSTA
              146   FILE GENBANK
               78   FILE IFIPAT
               55   FILE JICST-EPLUS
              190   FILE LIFESCI
              175   FILE MEDLINE
                3   FILE NTIS
                3   FILE OCEAN
              229   FILE PASCAL
               10   FILE PROMT
              449   FILE SCISEARCH
               51   FILE TOXCENTER
              297   FILE USPATFULL
                6   FILE USPAT2
               16   FILE VETU
              129   FILE WPIDS
              129   FILE WPINDEX
L1               QUE MANNANASE
                 ---------

     FILE 'CAPLUS, BIOSIS, SCISEARCH, BIOTECHDS' ENTERED AT 13:50:27 ON 07 JAN
     2003

     FILE 'PASCAL, CABA, AGRICOLA' ENTERED AT 13:50:55 ON 07 JAN 2003
L2             6 S L1 AND MULTIDOMAIN
```

L3	0	S L1 AND ACIDOTHERMUS(W)CELLULOLYTICUS
L4	0	S L1 AND CELLULOLYTICUS
L5	1208	S L1 AND (CARBOHYDRATE(W)BINDING(W)DOMAIN) OR CBD
L6	1	S L5 AND GH5 OR (CBD III) OR (CBD II)
L7	8	S L5 AND MULTIDOMAIN
L8	5	DUP REM L7 (3 DUPLICATES REMOVED)

L10 ANSWER 23 OF 25 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
DUPLICATE

ACCESSION NUMBER: 1991-0485815 PASCAL

TITLE (IN ENGLISH): Cloning, sequence analysis, and expression in Escherichia coli of a gene coding for a .beta.-**mannanase** from the extremely thermophilic bacterium Caldocellum saccharolyticum

AUTHOR: LUETHI E.; NILA BHANA JASMAT; GRAYLING R. A.; LOVE D. R.; BERGQUIST P. L.

CORPORATE SOURCE: Univ. Auckland, cent. gene technology, dep. cellular molecular biology, Auckland, New Zealand

SOURCE: Applied and environmental microbiology, (1991), 57(3), 694-700, 40 refs.
ISSN: 0099-2240 CODEN: AEMIDF

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-7195, 354000017545150130; INIST, 354000017545150130

AB A .lambda. recombinant phage expressing .beta.-**mannanase** activity in Escherichia coli has been isolated from a genomic library of the extremely thermophilic anaerobe 'Caldocellum saccharolyticum.' The gene was cloned into pBR322 on a 5-kb BamHI fragment, and its location was obtained by deletion analysis. The sequence of a 2,1-kb fragment containing the **mannanase** gene has been determined. One open reading frame was found which could code for a protein of M.sub.r 38,904. The **mannanase** gene (**manA**) was overexpressed in E. coli by cloning the gene downstream from the lacZ promoter of pUC18

L10 ANSWER 21 OF 25 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED.
ACCESSION NUMBER: 1993-0161687 PASCAL
TITLE (IN ENGLISH): The .beta.-**mannanase** from Caldocellum saccharolyticum is part of a multidomain enzyme
AUTHOR: GIBBS M. D.; SAUL D. J.; LUETHI E.; BERGQUIST P. L.
CORPORATE SOURCE: Univ. Auckland, cent. gene technology, dep. cellular molecular biology, Auckland, New Zealand
SOURCE: Applied and environmental microbiology, (1992), 58(12), 3864-3867, 18 refs.
ISSN: 0099-2240 CODEN: AEMIDF
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7195, 354000032511890140
AB The complete sequence of a .beta.-**mannanase** gene from an anaerobic extreme thermophile was determined, and it shows that the expressed protein consists of two catalytic domains and two binding domains separated by spacer regions rich in proline and threonine residues. The amino-terminal catalytic domain has .beta.-**mannanase** activity, and the carboxy-terminal domain acts as an endoglucanase. Neither domain shows homology with any other cellulase or hemicellulase sequence at the nucleic acid or protein level